## Figure 1.

- 1 acquire data
- 2 process signal
- 3 separate colors
- 4 remove primers
- 5 track sizes
- 6 extract profiles

Figure 2.

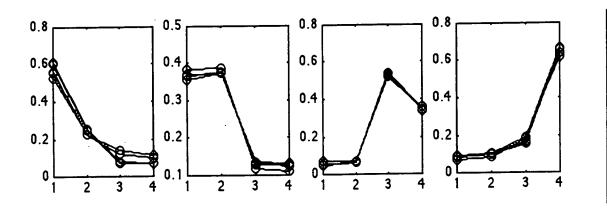


Figure 3.

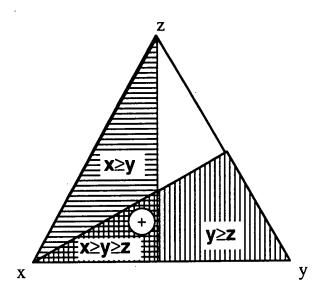


Figure 4.

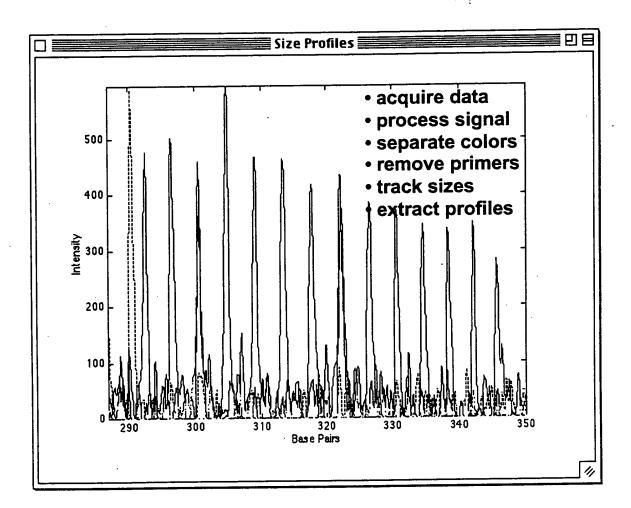


Figure 5.

7 derive allelic ladder
8 transform coordinates
9 quantitate trace
10 analyze data

Figure 6.

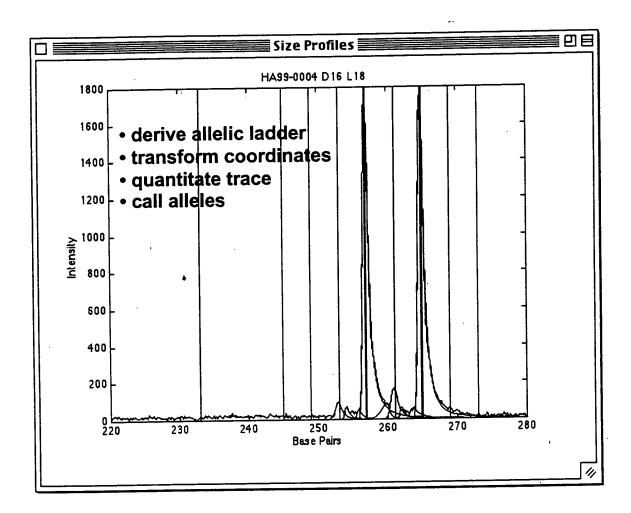


Figure 7.

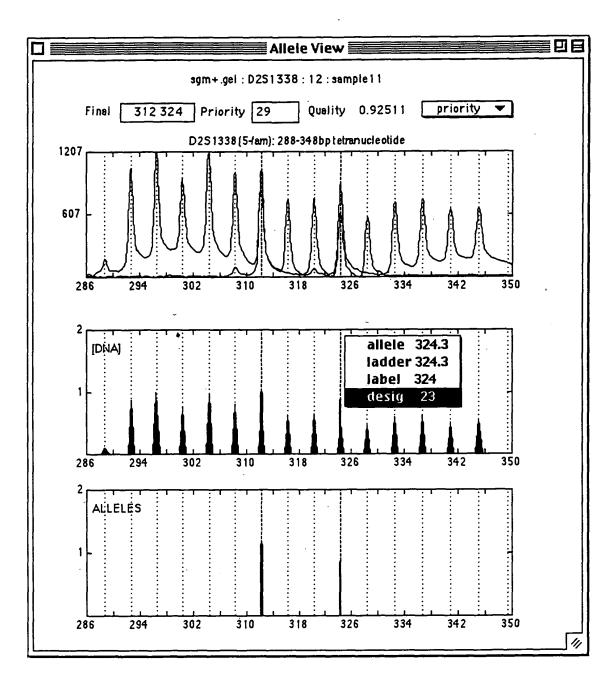


Figure 8.

CENOTYPES   Label   Designation   Allele Size   Ladder Size   Deviation	sgn+.ge]	L sample31 (1	L33): D2S1338			
Label   Designation   AlleleSize   LadderSize   Deviation	~~~	ne				
300 17 300.4 300.4 +0.0 324 23 324.3 324.3 +0.0  QUALITY Score = 0.0000  RHLES FIRED Number fired = 2 > peak centering The designated peaks should comprise a certain percentage of the signal. This profile's designated peaks contain less than that percentage. > third peak One or two peaks should contain most of the INVA signal. In this genotype, a third peak contained too much INVA signal.  PEAKS  Label Size Height Area PeakFit 296 296.6 51.3 35.9 0.8165 297 297.9 33.9 17.9 0.8014 300 300.4 523.1 249.2 0.9249 302 301.9 387.4 187.6 0.9355 320 320.5 23.1 16.2 0.7864 321 321.6 21.7 9.5 0.8252 324 324.3 380.3 210.9 0.9328			n AlleleSize	LadderSize	Deviation	
QUALITY Score = 0.0000  RULES FIRED  Number fired = 2  > peak centering  * The designated peaks should comprise a certain percentage of the signal.  This profile's designated peaks contain less than that percentage.  > third peak One or two peaks should contain most of the INVA signal.  In this genotype, a third peak contained too much INVA signal.  PEAKS  Label Size Height Area PeakFit 296 296.6 51.3 35.9 0.8165 297 297.9 33.9 .17.9 0.8014 300 300.4 523.1 249.2 0.9249 302 301.9 387.4 187.6 0.9355 320 320.5 23.1 16.2 0.7864 321 321.6 21.7 9.5 0.8252 324 324.3 380.3 210.9 0.9328				300.4	+0.0	
Score = 0.0000  NULES FIRED  Number fired = 2  > peak centering  The designated peaks should comprise a certain percentage of the signal.  This profile's designated peaks contain less than that percentage.  > third peak One or two peaks should contain most of the INVA signal.  In this genotype, a third peak contained too much INVA signal.  PEAKS  Label Size Height Area PeakFit 296 296.6 51.3 35.9 0.8165 297 297.9 33.9 17.9 0.8014 300 300.4 523.1 249.2 0.9249 302 301.9 387.4 187.6 0.9355 320 320.5 23.1 16.2 0.7864 321 321.6 21.7 9.5 0.8252 324 324.3 380.3 210.9 0.9328	• • •			324.3	+0.0	
RILES FIRED  Number fired = 2  > peak centering  The designated peaks should comprise a certain percentage of the signal.  This profile's designated peaks contain less than that percentage.  > third peak  One or two peaks should contain most of the INA signal.  In this genotype, a third peak contained too much INA signal.  PEAKS  Label Size Height Area PeakFit  296 296.6 51.3 35.9 0.8165  297 297.9 33.9 17.9 0.8014  300 300.4 523.1 249.2 0.9249  302 301.9 387.4 187.6 0.9355  320 320.5 23.1 16.2 0.7864  321 321.6 21.7 9.5 0.8252  324 324.3 380.3 210.9 0.9328	YTLIAND					
Number fired = 2 > peak centering The designated peaks should comprise a certain percentage of the signal. This profile's designated peaks contain less than that percentage. > third peak One or two peaks should contain most of the DNA signal. In this genotype, a third peak contained too much DNA signal.  PEAKS Label Size Height Area PeakFit 2% 2%6.6 51.3 35.9 0.8165 2%7 2%7.9 33.9 17.9 0.8014 300 300.4 523.1 249.2 0.9249 302 301.9 3%7.4 1%7.6 0.9355 320 320.5 23.1 16.2 0.7864 321 321.6 21.7 9.5 0.8252 324 324.3 380.3 210.9 0.9328	•					
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PEAKS  Label Size Height Area PeakFit  296 296.6 51.3 35.9 0.8165  297 297.9 33.9 17.9 0.8014  300 300.4 523.1 249.2 0.9249  302 301.9 387.4 187.6 0.9355  320 320.5 23.1 16.2 0.7864  321 321.6 21.7 9.5 0.8252  324 324.3 380.3 210.9 0.9328	The des This pr	ofile's desi Deak	gmated peaks o	contain less the	in that percentage.	
Label         Size         Heright         Area         PeakFit           296         296.6         51.3         35.9         0.8165           297         297.9         33.9         17.9         0.8014           300         300.4         523.1         249.2         0.9249           302         301.9         387.4         187.6         0.9355           320         320.5         23.1         16.2         0.7864           321         321.6         21.7         9.5         0.8252           324         324.3         380.3         210.9         0.9328	The des This pr >third	ofile's desi peak two peaks sh	gnated peaks o would contain m	contain less the rost of the DNA	in that percentage.  signal.	
Label         Size         Heright         Area         PeakFit           296         296.6         51.3         35.9         0.8165           297         297.9         33.9         17.9         0.8014           300         300.4         523.1         249.2         0.9249           302         301.9         387.4         187.6         0.9355           320         320.5         23.1         16.2         0.7864           321         321.6         21.7         9.5         0.8252           324         324.3         380.3         210.9         0.9328	The des This pr >third	ofile's desi peak two peaks sh	gnated peaks o would contain m	contain less the rost of the DNA	in that percentage.  signal.	
296     296.6     51.3     35.9     0.8165       297     297.9     33.9     17.9     0.8014       300     300.4     523.1     249.2     0.9249       302     301.9     387.4     187.6     0.9355       320     320.5     23.1     16.2     0.7864       321     321.6     21.7     9.5     0.8252       324     324.3     380.3     210.9     0.9328	The des This pr >third One or In this	ofile's desi peak two peaks sh	gnated peaks o would contain m	contain less the rost of the DNA	in that percentage.  signal.	
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302     301.9     387.4     187.6     0.9355       320     320.5     23.1     16.2     0.7864       321     321.6     21.7     9.5     0.8252       324     324.3     380.3     210.9     0.9328	The des This pr >third One or In this PEAKS Label 2%	ofile's desi peak two peaks sh genotype, a Size 296.6	grated peaks of could contain m third peak of Height 51.3	contain less the cost of the DNA entained too mu Area 35.9	signal.  ch INA signal.  PeakFit  0.8165	
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320.7	The des This prothind One or In this PEAKS Label 296 297 300 302 320 321	ofile's desi peak two peaks sh genotype, a Size 296.6 297.9 300.4 301.9 320.5 321.6	grated peaks of mould contain many third peak of Height 51.3 33.9 523.1 387.4 23.1 21.7	Area 35.9 17.9 249.2 187.6 16.2 9.5	signal. signal. PeakFit 0.8165 0.8014 0.9249 0.9355 0.7864 0.8252	
	The des This prothind One or In this PEAKS Label 296 297 300 302 320 321 324	ofile's desi peak two peaks sh genotype, a Size 296.6 297.9 300.4 301.9 320.5 321.6 324.3	grated peaks of could contain mathrid peak of Height 51.3 33.9 523.1 387.4 23.1 21.7 380.3	Area 35.9 17.9 249.2 187.6 16.2 9.5 210.9	rich that percentage.  signal.  ch DNA signal.  PeakFit  0.8165  0.8014  0.9249  0.9355  0.7864  0.8252  0.9328	
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	The des This prothind One or In this PEAKS Label 296 297 300 302 320 321 324	ofile's desi peak two peaks sh genotype, a Size 296.6 297.9 300.4 301.9 320.5 321.6 324.3	grated peaks of could contain mathrid peak of Height 51.3 33.9 523.1 387.4 23.1 21.7 380.3	Area 35.9 17.9 249.2 187.6 16.2 9.5 210.9	rich that percentage.  signal.  ch DNA signal.  PeakFit  0.8165  0.8014  0.9249  0.9355  0.7864  0.8252  0.9328	
	The des This prothind One or In this PEAKS Label 296 297 300 302 320 321 324	ofile's desi peak two peaks sh genotype, a Size 296.6 297.9 300.4 301.9 320.5 321.6 324.3	grated peaks of could contain mathrid peak of Height 51.3 33.9 523.1 387.4 23.1 21.7 380.3	Area 35.9 17.9 249.2 187.6 16.2 9.5 210.9	rich that percentage.  signal.  ch DNA signal.  PeakFit  0.8165  0.8014  0.9249  0.9355  0.7864  0.8252  0.9328	

Figure 9.

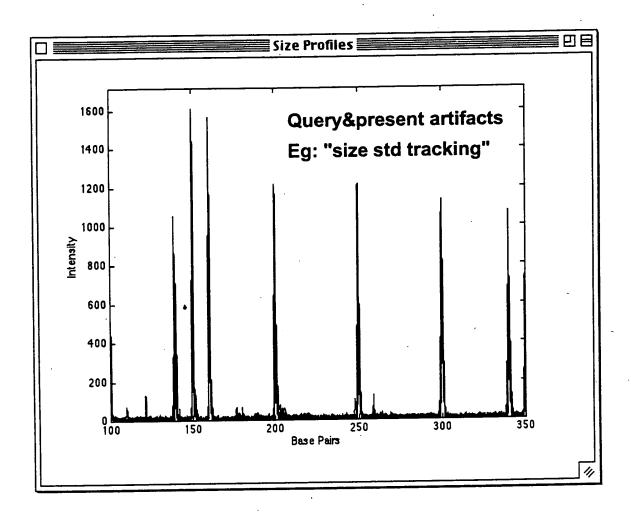


Figure 10.

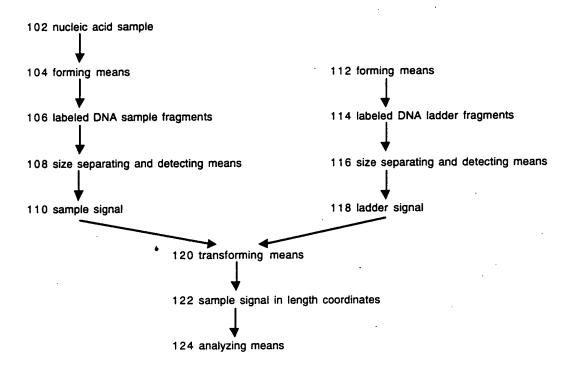


Figure 11.

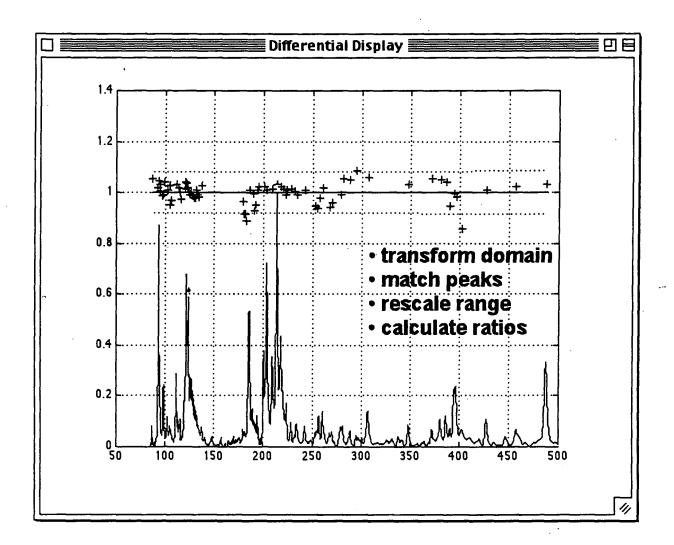


Figure 12

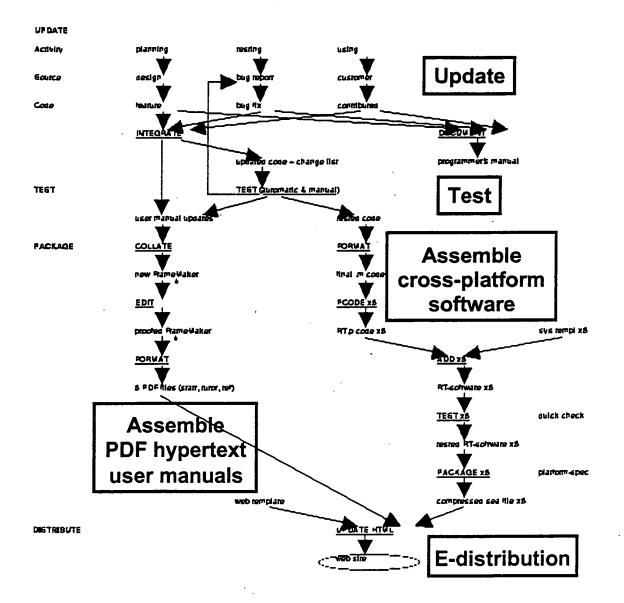


Figure 13

			ab	orCost 🔀			旧
	A	В	С	D	Ε	F	
20 21 22 23	PEOPLE COST PER GENOTYPE	\$1,02 <del>4</del> ,000 \$1.02					
24	Breakdown	per person			per day	peryear	
26	salary benefits	\$25,000 \$6,250		Throughput runs	4,000	2,000 1,000,000	
27 28 29	space computer	\$2,000 \$2,000 \$10,000		genotypes Scoring	4,000	1,000,000	
30 31	software management overhead	\$6,250 \$12,500		calls/person	500	125,000	
32 33	COST	\$64,000		PEOPLE	16		
34 35	Assumptions benefit rate	0.25		Assumptions genotypes/run	500		
36	sqfeet/person	100 \$20		days/year people/call	250		
37 38 39 40	cost/sqfoot yr managing rate overhead rate	0.25 0.50		heobietem			
1	                 LaborCos	st /				Þ	111

Figure 14.

